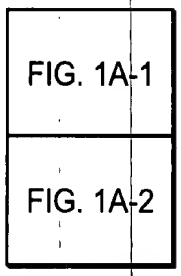


FIG. 1A

```
GAATTCCCCCAACAGAGCCAAGCTCTCCATCTAGTGGACAGGGAAGCTAGCAGCAAACC     39 (UPPER: SEQ ID NO.: 1)
                                                                 19 (LOWER: SEQ ID NO.: 4)

TTCCCTTCACTACAAAACTTCATTGCTTGGCCAAAAAGAGAGTTAATTCAATGTAGACAT    119
                                                                 39

CTATGTAGGCAATTAAAAACCTATTGATGTATAAAACAGTTTGCATTCATGGAGGGCAAC    179
                                                                 59

TAAATACATTCTAGGACTTTATAAAAGATCACTTTTTATTTATGCACAGGGTGGAACAAG    239
                                                                 79

ATGGATTATCAAGTGTCAAGTCCAATCTATGACATCAATTATTATACATCGGAGCCCTGC    299
 M  D  Y  Q  V  S  S  P  I  Y  D  I  N  Y  Y  T  S  E  P  C     99
```

FIG. 1A-1

```
CAAAAAATCAATGTGAAGCAAATCGCAGCCCGCCTCCTGCCTCCGCTCTACTCACTGGTG     359
 Q  K  I  N  V  K  Q  I  A  A  R  L  L  P  P  L  Y  S  L  V     119

TTCATCTTTGGTTTTGTGGGCAACATGCTGGTCATCCTCATCCTGATAAACTGCAAAAGG     419
 F  I  F  G  F  V  G  N  M  L  V  I  L  I  L  I  N  C  K  R     139

CTGAAGAGCATGACTGACATCTACCTGCTCAACCTGGCCATCTCTGACCTGTTTTTCCTT     479
 L  K  S  M  T  D  I  Y  L  L  N  L  A  I  S  D  L  F  F  L     159

CTTACTGTCCCCTTCTGGGCTCACTATGCTGCCGCCCAGTGGGACTTTGGAAATACAATG     539
 L  T  V  P  F  W  A  H  Y  A  A  A  Q  W  D  F  G  N  T  M     179

TGTCAACTCTTGACAGGGCTCTATTTTATAGGCTTCTTCTCTGGAATCTTCTTCATCATC     599
 C  Q  L  L  T  G  L  Y  F  I  G  F  F  S  G  I  F  F  I  I     199

CTCCTGACAATCGATAGGTACCTGGCTGTCGTCCATGCTGTGTTTGCTTTAAAAGCCAGG     659
 L  L  T  I  D  R  Y  L  A  V  V  H  A  V  F  A  L  K  A  R     219

ACGGTCACCTTTGGGGTGGTGACAAGTGTGATCACTTGGGTGGTGGCTGTGTTTGCGTCT     719
 T  V  T  F  G  V  V  T  S  V  I  T  W  V  V  A  V  F  A  S     239

CTCCCAGGAATCATCTTTACCAGATCTCAAAAAGAAGGTCTTCATTACACCTGCAGCTCT     779
 L  P  G  I  I  F  T  R  S  Q  K  E  G  L  H  Y  T  C  S  S     259

CATTTTCCATACA
 H  F  P  Y
```

FIG. 1A-2

FIG. 1B-1

FIG. 1B-2

FIG. 1B

```
GAATTCCCCCAACAGAGCCAAGCTCTCCATCTAGTGGACAGGGAAGCTAGCAGCAAACC    59 (UPPER: SEQ ID NO.: 2)
                                                               19 (LOWER: SEQ ID NO.: 5)

TTCCCTTCACTACAAAACTTCATTGCTTGGCCAAAAAGAGAGTTAATTCAATGTAGACAT  119
                                                               39

CTATGTAGGCAATTAAAAACCTATTGATGTATAAAACAGTTTGCATTCATGGAGGGCAAC  179
                                                               59

TAAATACATTCTAGGACTTTATAAAAGATCACTTTTTATTTATGCACAGGGTGGAACAAG  239
                                                               79

ATGGATTATCAAGTGTCAAGTCCAATCTATGACATCAATTATTATACATCGGAGCCCTGC  299
 M  D  Y  Q  V  S  S  P  I  Y  D  I  N  Y  Y  T  S  E  P  C    99
```

FIG. 1B-1

```
CAAAAAATCAATGTGAAGCAAATCGCAGCCCGCCTCCTGCCTCCGCTCTACTCACTGGTG   359
 Q  K  I  N  V  K  Q  I  A  A  R  L  L  P  P  L  Y  S  L  V    119

TTCATCTTTGGTTTTGTGGGCAACATGCTGGTCATCCTCATCCTGATAAACTGCAAAAGG   419
 F  I  F  G  F  V  G  N  M  L  V  I  L  I  L  I  N  C  K  R    139

CTGAAGAGCATGACTGACATCTACCTGCTCAACCTGGCCATCTCTGACCTGTTTTTCCTT   479
 L  K  S  M  T  D  I  Y  L  L  N  L  A  I  S  D  L  F  F  L    159

CTTACTGTCCCCTTCTGGGCTCACTATGCTGCCGCCCAGTGGGACTTTGGAAATACAATG   539
 L  T  V  P  F  W  A  H  Y  A  A  A  Q  W  D  F  G  N  T  M    179

TGTCAACTCTTGACAGGGCTCTATTTTATAGGCTTCTTCTCTGGAATCTTCTTCATCATC   599
 C  Q  L  L  T  G  L  Y  F  I  G  F  F  S  G  I  F  F  I  I    199

CTCCTGACAATCGATAGGTACCTGGCTGTCGTCCATGCTGTGTTTGCTTTAAAAGCCAGG   659
 L  L  T  I  D  R  Y  L  A  V  V  H  A  V  F  A  L  K  A  R    219

ACGGTCACCTTTGGGGTGGTGACAAGTGTGATCACTTGGGTGGTGGCTGTGTTTGCGTCT   719
 T  V  T  F  G  V  V  T  S  V  I  T  W  V  V  A  V  F  A  S    239

CTCCCAGGAATCATCTTTACCAGATCTCAAAAAGAAGGTCTTCATTACACCTGCAGCTCT   779
 L  P  G  I  I  F  T  R  S  Q  K  E  G  L  H  Y  T  C  S  S    259

CATTTTCCATACAGTCAGTATCAATTCTGGAAGAATTTCCAGACATTAAAGATAGTCATC   839
 H  F  P  Y  S  Q  Y  Q  F  W  K  N  F  Q  T  L  K  I  V  I    279
```

FIG. 1B-2

```
TTGGGGCTGGTCCTGCCGCTGCTTGTCATGGTCATCTGCTACTCGGGAATCCTAAAAACT   899
 L  G  L  V  L  P  L  L  V  M  V  I  C  Y  S  G  I  L  K  T    299

CTGCTTCGGTGTCGAAATGAGAAGAAGAGGCACAGGGCTGTGAGGCTTATCTTCACCATC   959
 L  L  R  C  R  N  E  K  K  R  H  R  A  V  R  L  I  F  T  I    319

ATGATTGTTTATTTTCTCTTCTGGGCTCCCTACAACATTGTCCTTCTCCTGAACACCTTC  1019
 M  I  V  Y  F  L  F  W  A  P  Y  N  I  V  L  L  L  N  T  F    339

CAGGAATTCTTTGGCCTGAATAATTGCAGTAGCTCTAACAGGTTGGACCAAGCTATGCAG  1079
 Q  E  F  F  G  L  N  N  C  S  S  S  N  R  L  D  Q  A  M  Q    359

GTGACAGAGACTCTTGGGATGACGCACTGCTGCATCAACCCCATCATCTATGCCTTTGTC  1139
 V  T  E  T  L  G  M  T  H  C  C  I  N  P  I  I  Y  A  F  V    379

GGGGAGAAGTTCAGAAACTACCTCTTAGTCTTCTTCCAAAAGCACATTGCCAAACGCTTC  1199
 G  E  K  F  R  N  Y  L  L  V  F  F  Q  K  H  I  A  K  R  F    399

TGCAAATGCTGTTCTATTTTCCAGCAAGAGGCTCCCGAGCGAGCAAGCTCAGTTTACACC  1259
 C  K  C  C  S  I  F  Q  Q  E  A  P  E  R  A  S  S  V  Y  T    419

CGATCCACTGGGGAGCAGGAAATATCTGTGGGCTTGTGACACGGACTCAAGTGGGCTGGT  1319
 R  S  T  G  E  Q  E  I  S  V  G  L  *                         439

GACCCAGTCAGAGTTGTGCACATGGCTTAGTTTTCATACACAGCCTGGGCTGGGGGTNGG  1379
                                                                459

TTGGNNGAGGTCTTTTTTAAAAGGAAGTTACTGTTATAGAGGGTCTAAGATTCATCCATT  1439
                                                                479

TATTTGGCATCTGTTTAAAGTAGATTAGATCCGAATTC
```

FIG. 1B-3

FIG. 1D-1

FIG. 1D-2

FIG. 1D

```
GAATTCCCCCAACAGAGCCAAGCTCTCCATCTAGTGGACAGGGAAGCTAGCAGCAAACC      59 (UPPER: SEQ ID NO. 3)
                                                                 19 (LOWER: SEQ ID NO. 6)

TTCCCTTCACTACAAAACTTCATTGCTTGGCCAAAAAGAGAGTTAATTCAATGTAGACAT     119
                                                                 39

CTATGTAGGCAATTAAAAACCTATTGATGTATAAAACAGTTTGCATTCATGGAGGGCAAC     179
                                                                 59

TAAATACATTCTAGGACTTTATAAAAGATCACTTTTTATTTATGCACAGGGTGGAACAAG     239
                                                                 79

ATGGATTATCAAGTGTCAAGTCCAATCTATGACATCAATTATTATACATCGGAGCCCTGC     299
 M  D  Y  Q  V  S  S  P  I  Y  D  I  N  Y  Y  T  S  E  P  C      99
```

FIG. 1D-1

```
CAAAAAATCAATGTGAAGCAAATCGCAGCCCGCCTCCTGCCTCCGCTCTACTCACTGGTG   359
 Q  K  I  N  V  K  Q  I  A  A  R  L  L  P  P  L  Y  S  L  V    119

TTCATCTTTGGTTTTGTGGGCAACATGCTGGTCATCCTCATCCTGATAAACTGCAAAAGG   419
 F  I  F  G  F  V  G  N  M  L  V  I  L  I  L  I  N  C  K  R    139

CTGAAGAGCATGACTGACATCTACCTGCTCAACCTGGCCATCTCTGACCTGTTTTTCCTT   479
 L  K  S  M  T  D  I  Y  L  L  N  L  A  I  S  D  L  F  F  L    159

CTTACTGTCCCCTTCTGGGCTCACTATGCTGCCGCCCAGTGGGACTTTGGAAATACAATG   539
 L  T  V  P  F  W  A  H  Y  A  A  A  Q  W  D  F  G  N  T  M    179

TGTCAACTCTTGACAGGGCTCTATTTTATAGGCTTCTTCTCTGGAATCTTCTTCATCATC   599
 C  Q  L  L  T  G  L  Y  F  I  G  F  F  S  G  I  F  F  I  I    199

CTCCTGACAATCGATAGGTACCTGGCTGTCGTCCATGCTGTGTTTGCTTTAAAAGCCAGG   659
 L  L  T  I  D  R  Y  L  A  V  V  H  A  V  F  A  L  K  A  R    219

ACGGTCACCTTTGGGGTGGTGACAAGTGTGATCACTTGGGTGGTGGCTGTGTTTGCGTCT   719
 T  V  T  F  G  V  V  T  S  V  I  T  W  V  V  A  V  F  A  S    239

CTCCCAGGAATCATCTTTACCAGATCTCAAAAAGAAGGTCTTCATTACACCTGCAGCTCT   779
 L  P  G  I  I  F  T  R  S  Q  K  E  G  L  H  Y  T  C  S  S    259

CATTTTCCATACATTAAAGATAGTCATCTTGGGGCTGGTCCTGCCGCTGCTTGTCATGGT   839
 H  F  P  Y  I  K  D  S  H  L  G  A  G  P  A  A  A  C  H  G    279
```

FIG. 1D-2

```
CATCTGCTACTCGGGAATCCTAAAAACTCTGCTTCGGTGTCGAAATGAGAAGAAGAGGCA   899
 H  L  L  L  G  N  P  K  N  S  A  S  V  S  K  *                299
CAGGGCTGTGAGGCTTATCTTCACCATCATGATTGTTTATTTTCTCTTCTGGGCTCCCTA   959
                                                               319
CAACATTGTCCTTCTCCTGAACACCTTCCAGGAATTCTTTGGCCTGAATAATTGCAGTAG  1019
                                                               339
CTCTAACAGGTTGGACCAAGCTATGCAGGTGACAGAGACTCTTGGGATGACGCACTGCTG  1079
                                                               359
CATCAACCCCATCATCTATGCCTTTGTCGGGGAGAAGTTCAGAAACTACCTCTTAGTCTT  1139
                                                               379
CTTCCAAAAGCACATTGCCAAACGCTTCTGCAAATGCTGTTCTATTTTCCAGCAAGAGGC  1199
                                                               399
TCCCGAGCGAGCAAGCTCAGTTTACACCCGATCCACTGGGGAGCAGGAAATATCTGTGGG  1259
                                                               419
CTTGTGACACGGACTCAAGTGGGCTGGTGACCCAGTCAGAGTTGTGCACATGGCTTAGTT  1319
                                                               439
TTCATACACAGCCTGGGCTGGGGGTNGGTTGGNNGAGGTCTTTTTTAAAAGGAAGTTACT  1379
                                                               459
GTTATAGAGGGTCTAAGATTCATCCATTTATTTGGCATCTGTTTAAAGTAGATTAGATCC  1439
                                                               479
GAATTC
```

8/20

FIG. 1D-3

FIG. 2A

FIG. 2B

FIG. 2

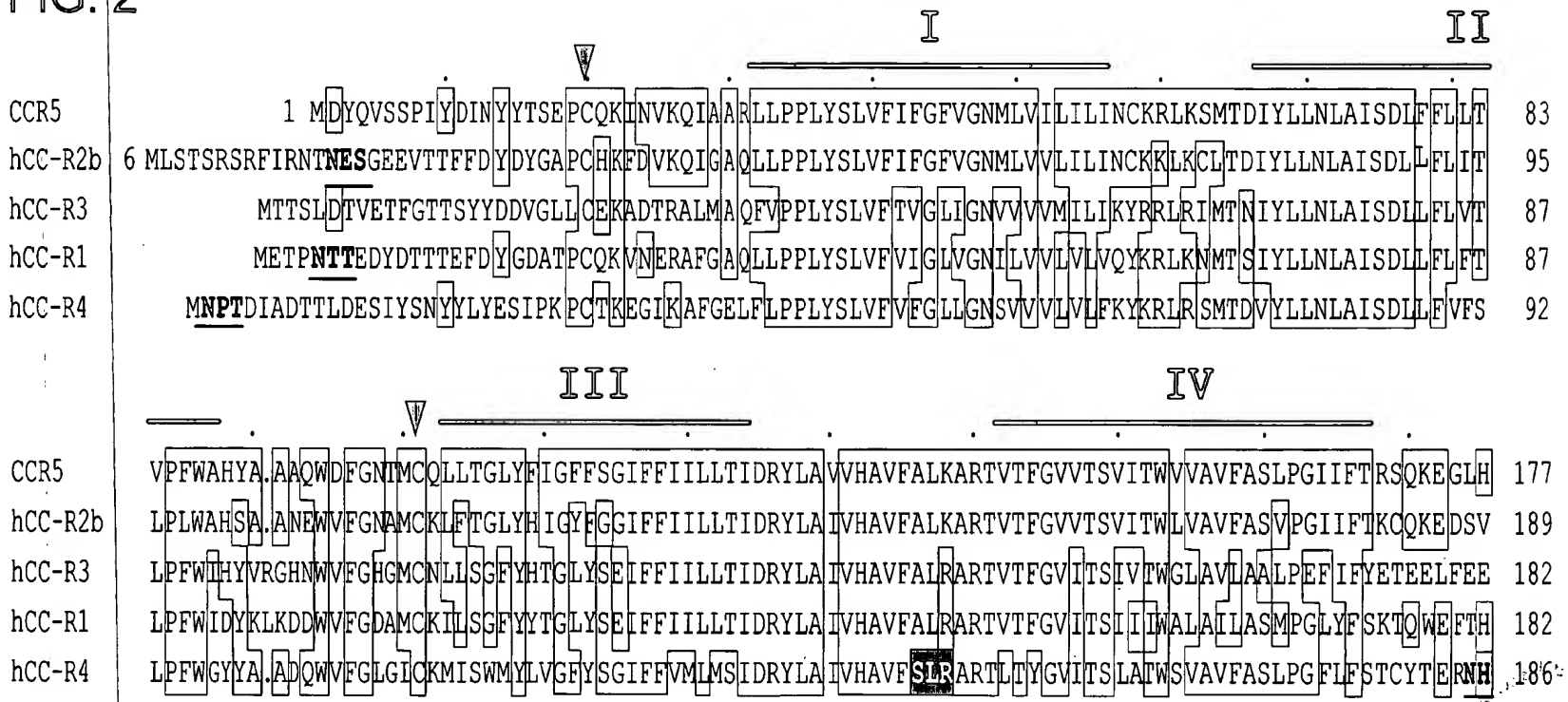


FIG. 2A

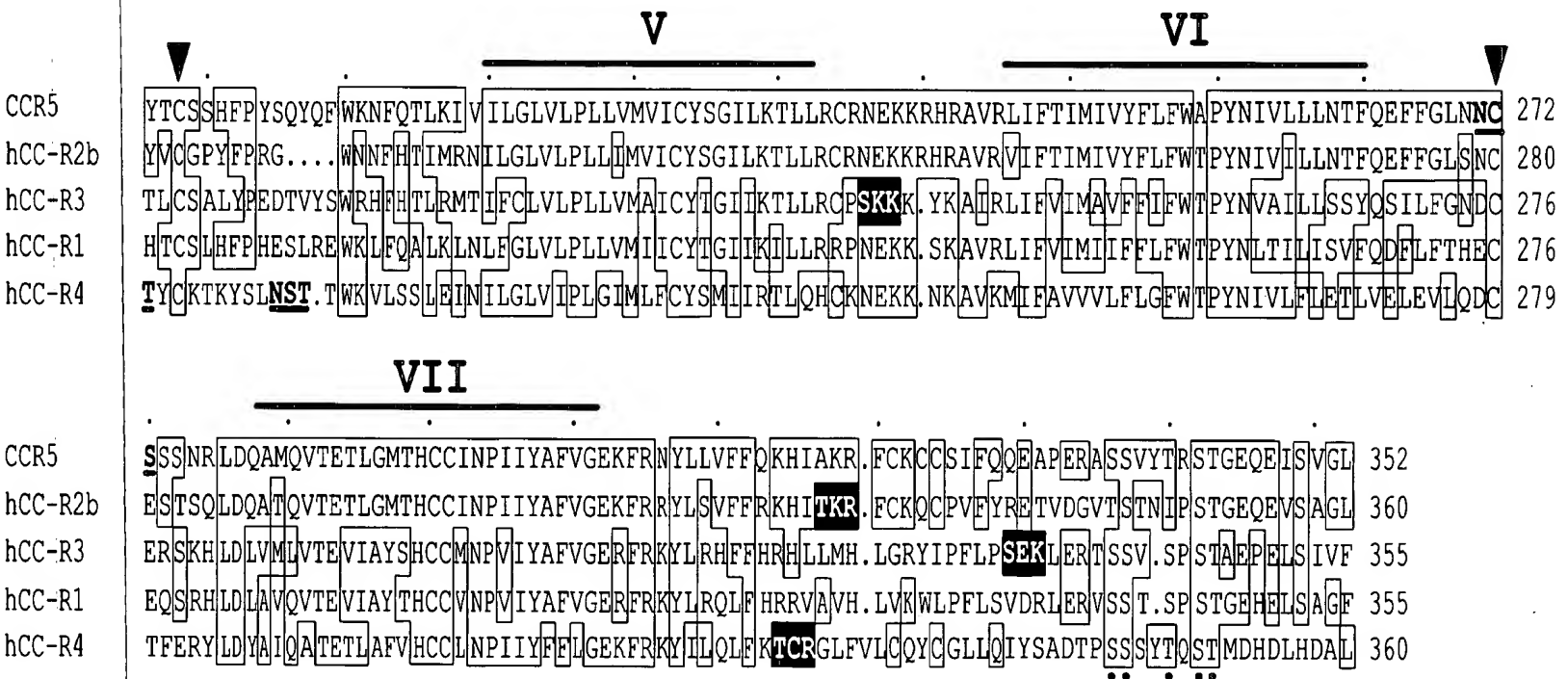


FIG. 2B

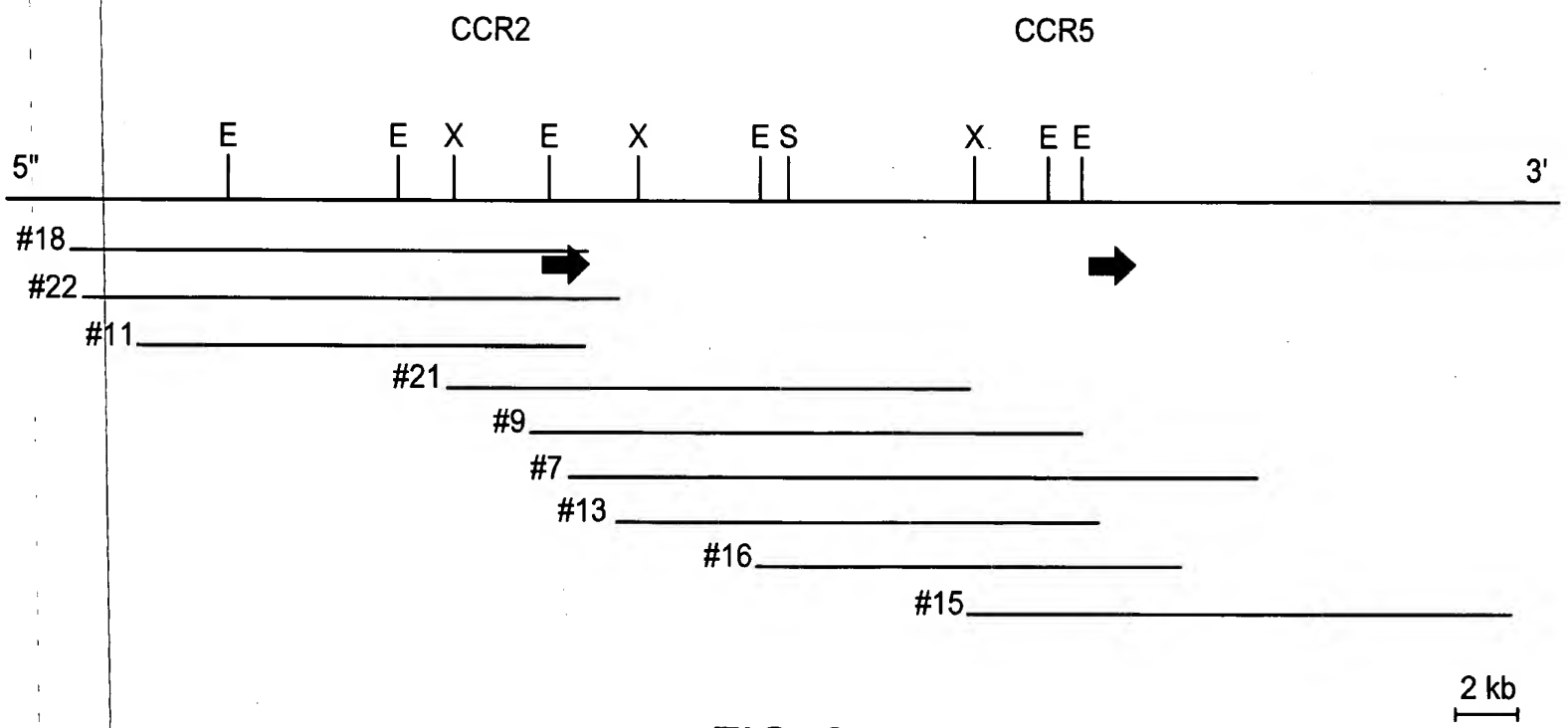


FIG. 3

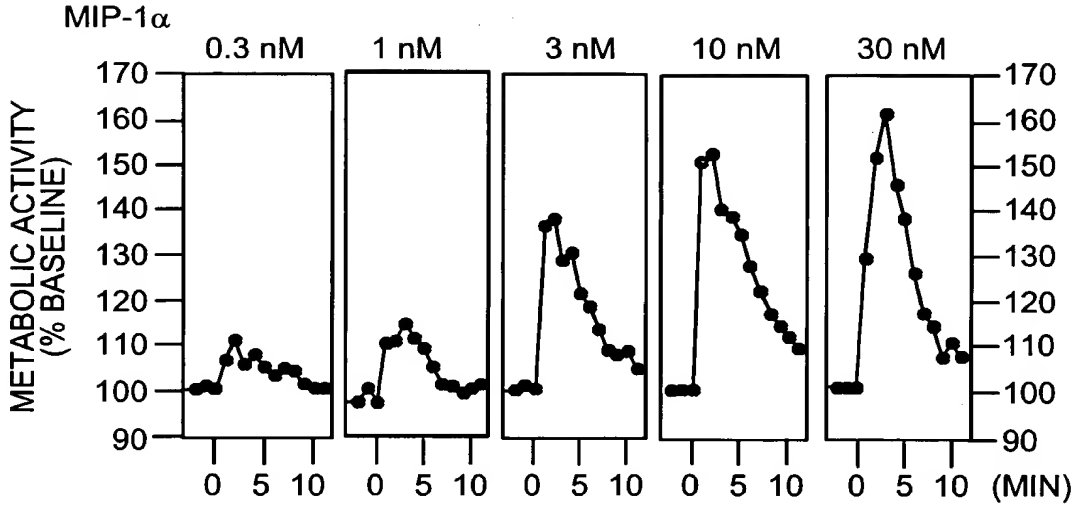


FIG. 4A

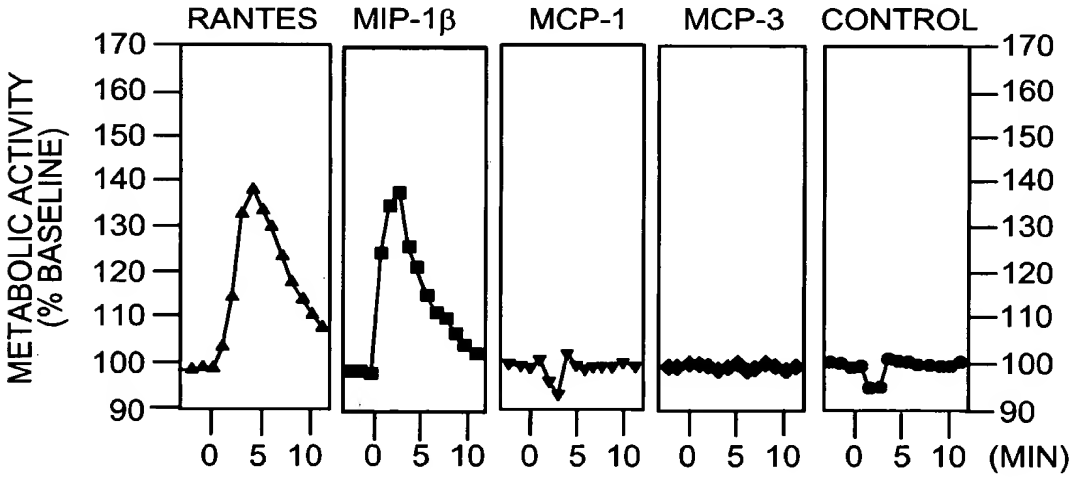


FIG. 4B

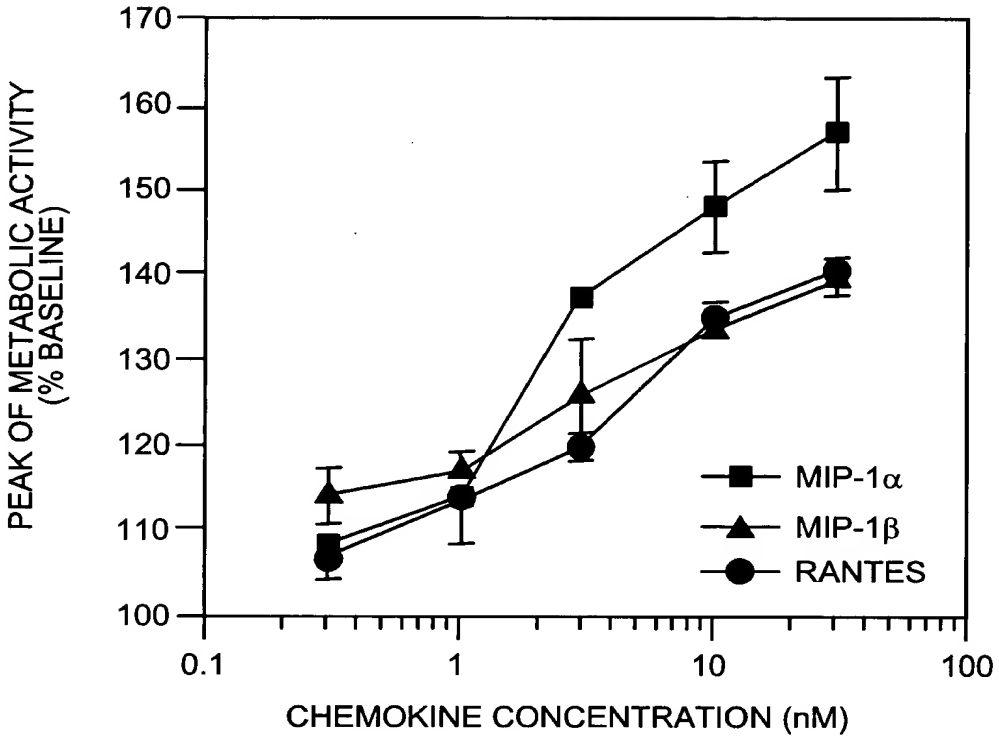


FIG. 4C

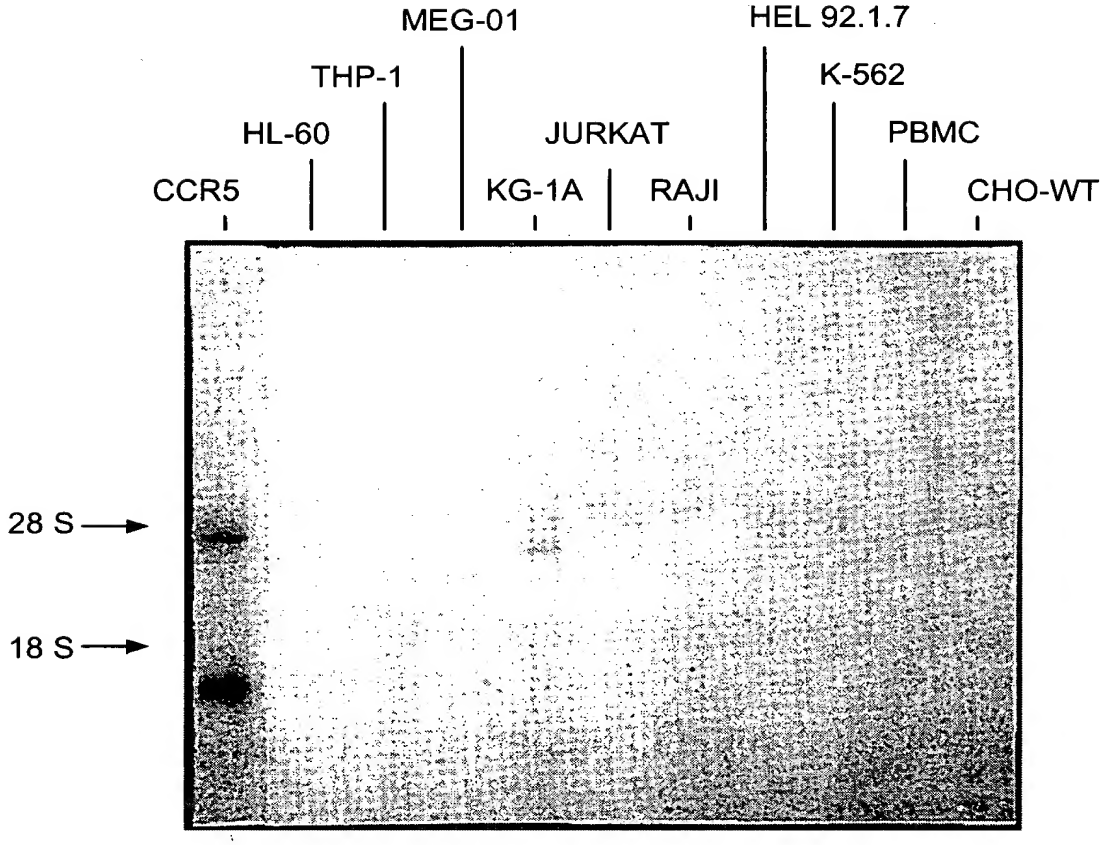


FIG. 5

FIG. 6A

FIG.6B

FIG. 6

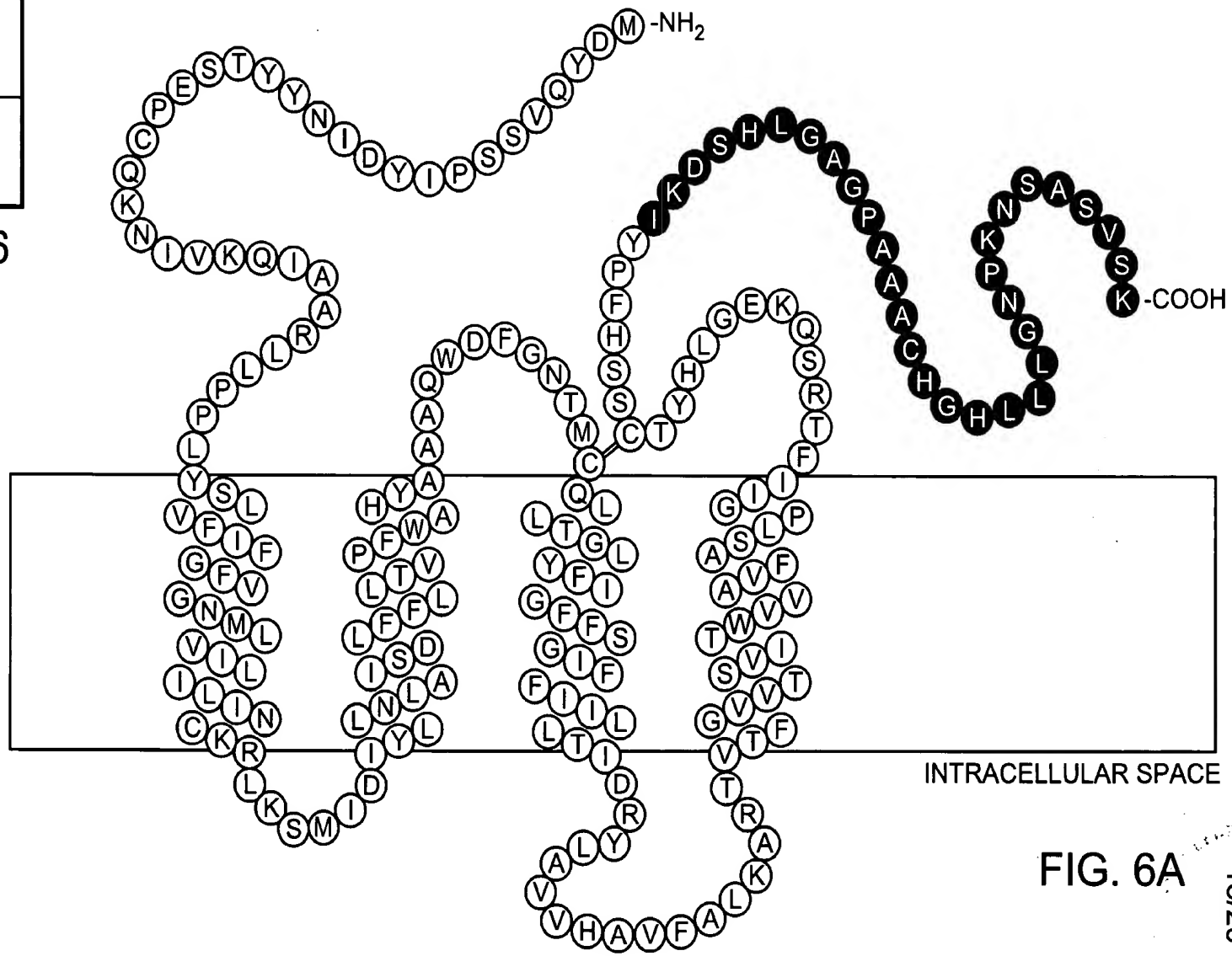


FIG. 6A

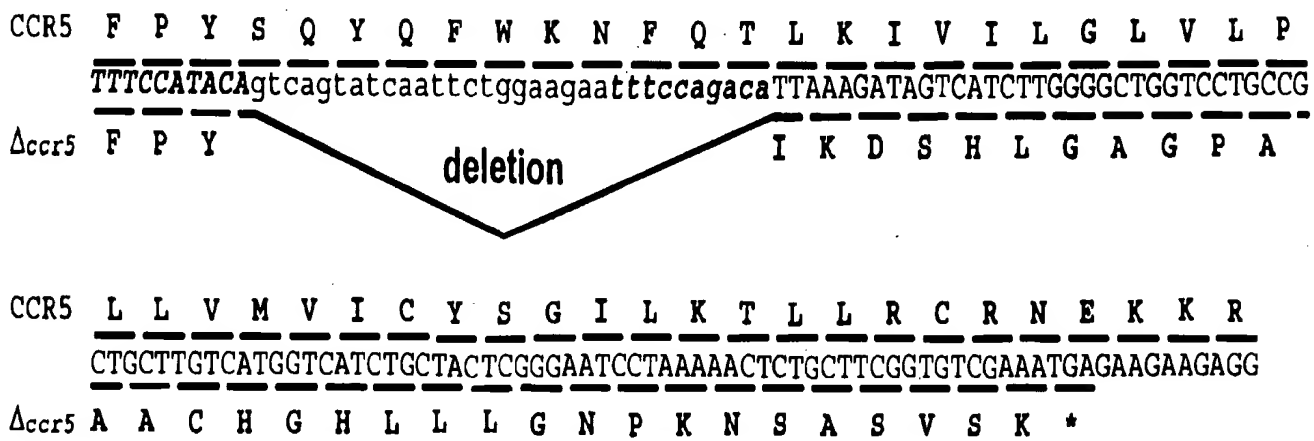


FIG. 6B

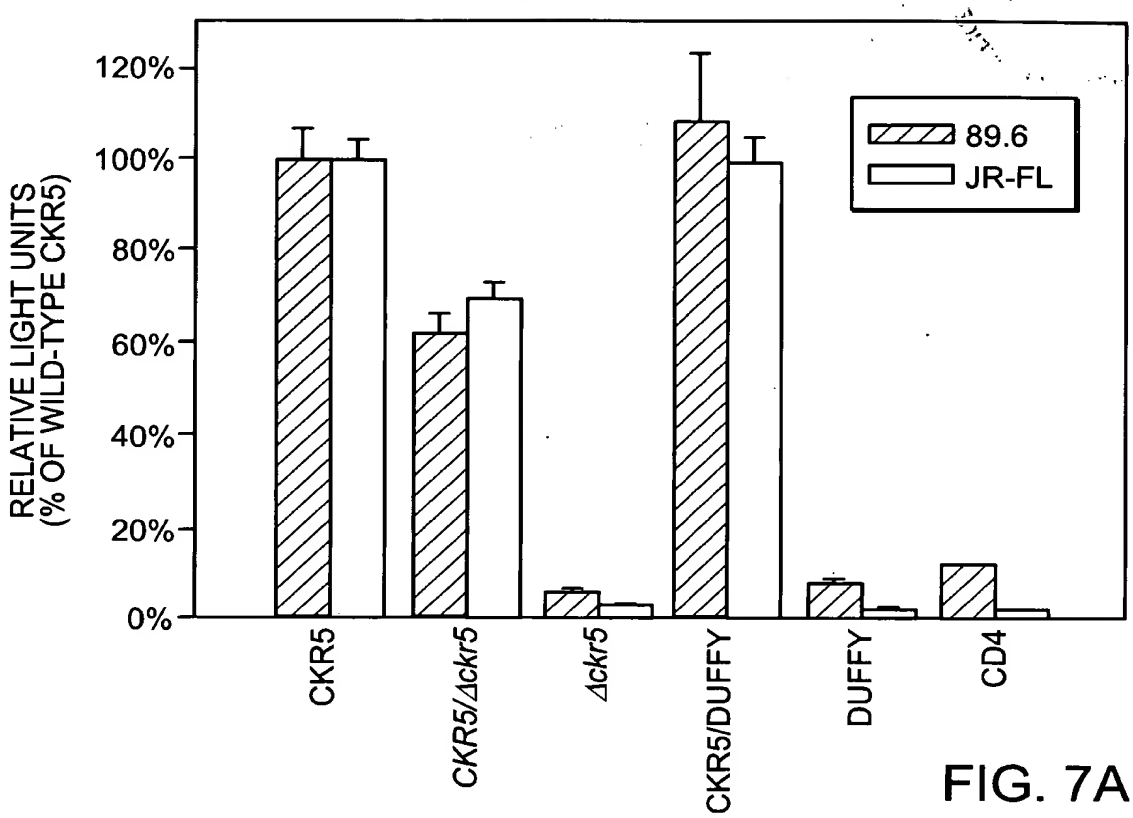


FIG. 7A

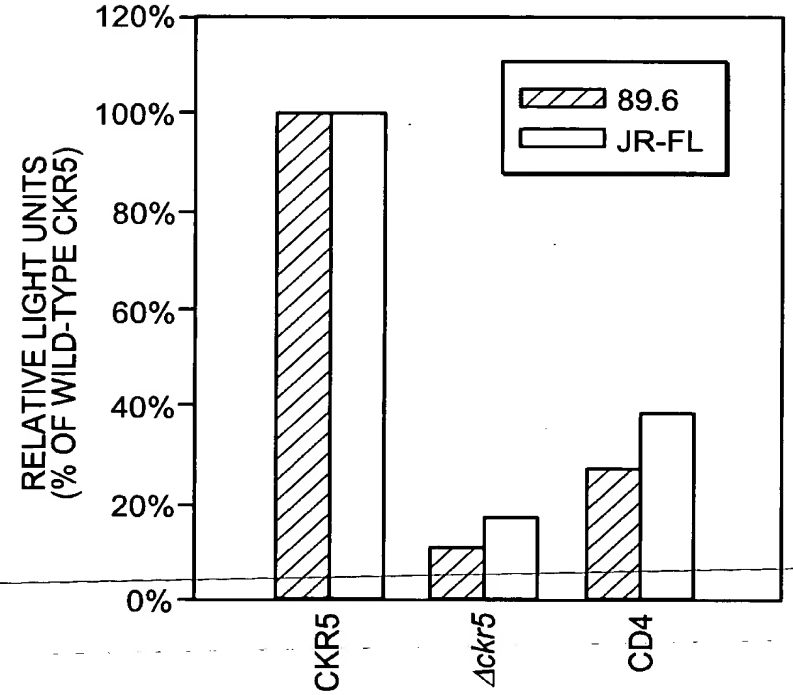


FIG. 7B

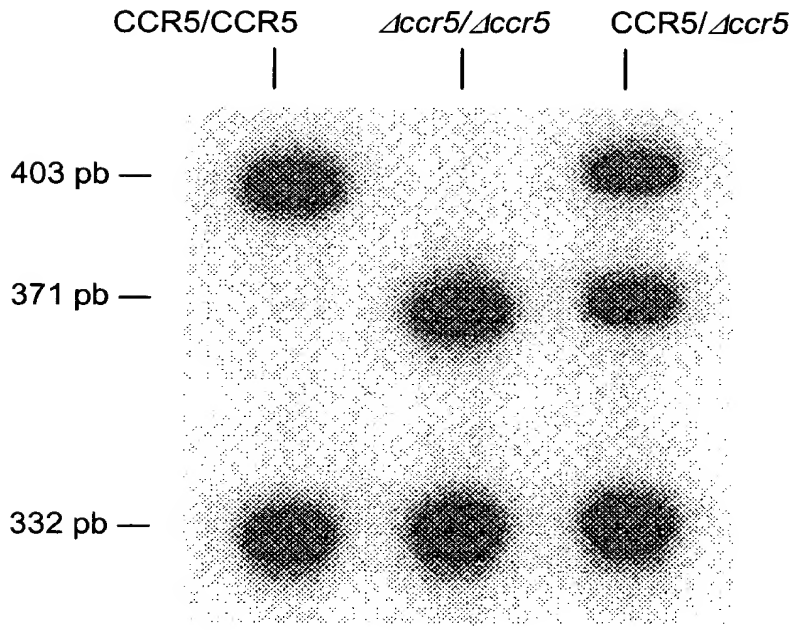
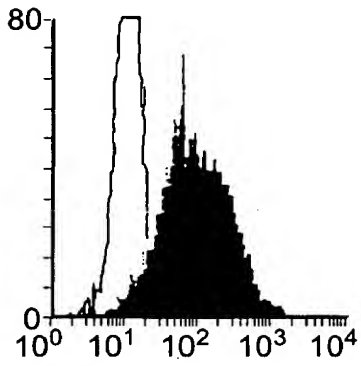
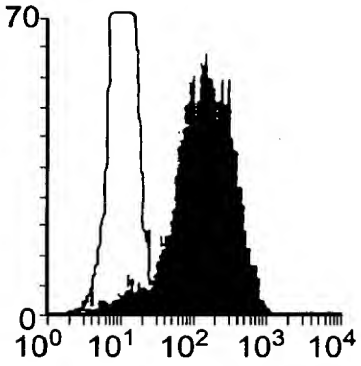


FIG. 8



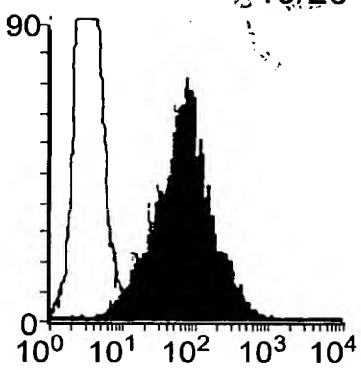
A0

FIG. 9A



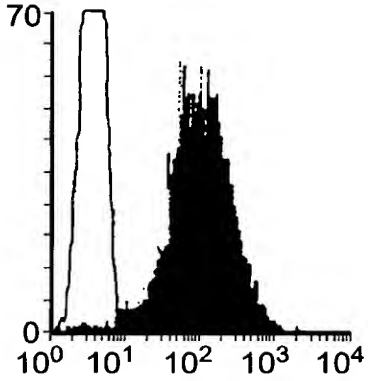
A1

FIG. 9B



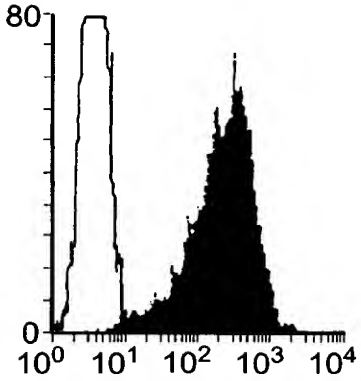
A2

FIG. 9C



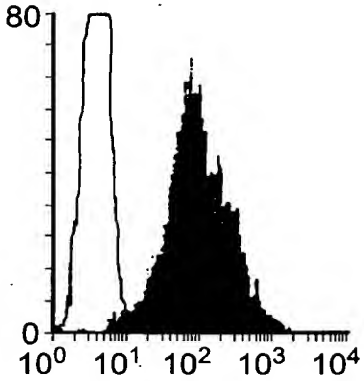
A5

FIG. 9D



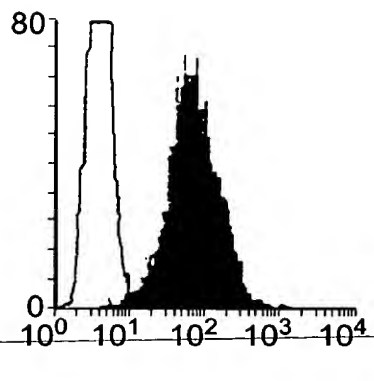
A4

FIG. 9E



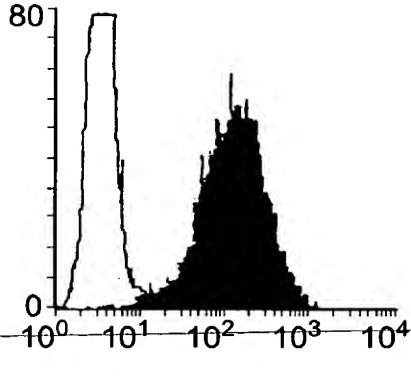
B0

FIG. 9F



B1

FIG. 9G



B3

FIG. 9H

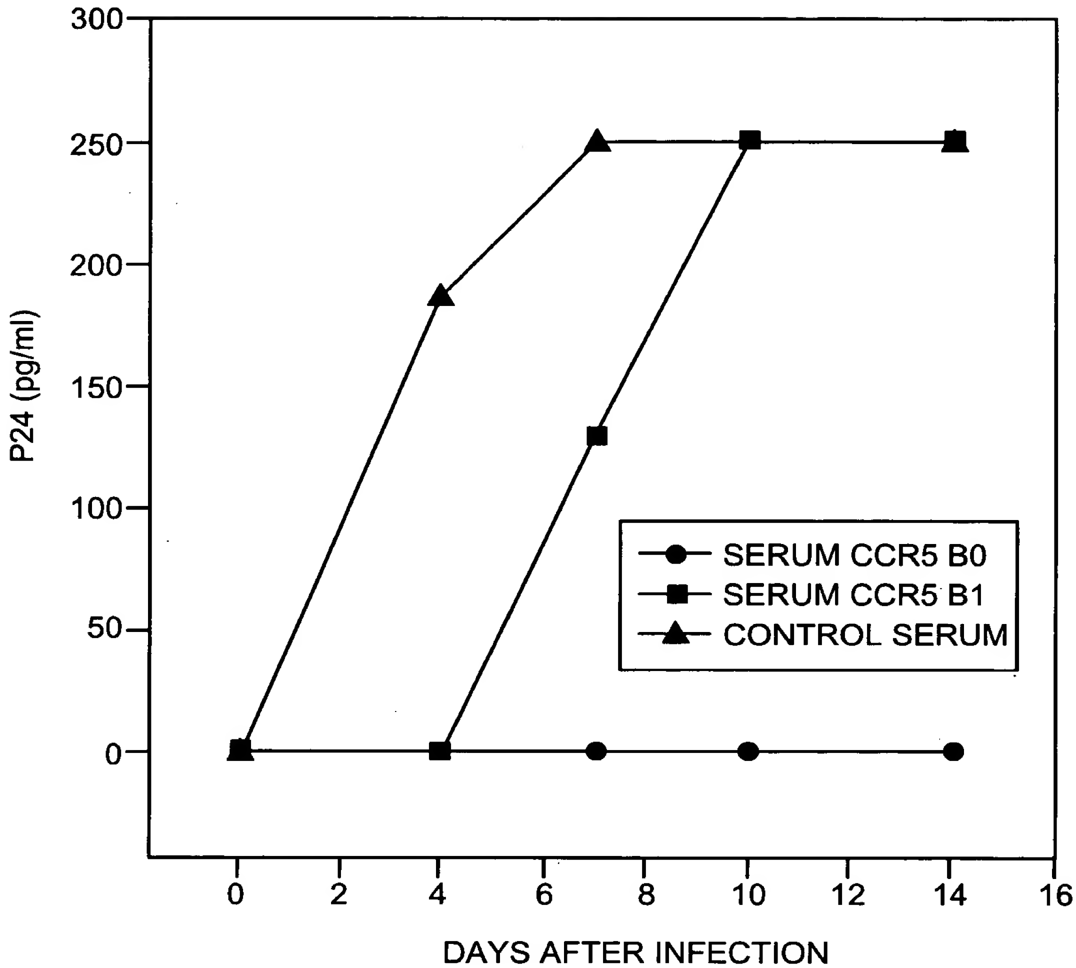

P24 (pg/ml)
300
250
200
150
100
50
0
DAYS AFTER INFECTION
0
2
4
6
8
10
12
14
16
SERUM CCR5 B0
SERUM CCR5 B1
CONTROL SERUM

FIG. 10